Untitled
GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 21:40:17 ; Search time 24770 Seconds
(without alignments)
12052.439 Million cell updates/sec

Title: US-09-242-772-116
Perfect score: 7313
Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcgtgcc 7313

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 45554873 seqs, 20411521753 residues

Word size : 0

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	7313	100.0	7313	18	US-09-242-772-116	Sequence 116, App
	2	7313	100.0	7313	41	US-09-948-941-30	Sequence 30, Appl
	3	7313	100.0	7313	41	US-09-949-003C-307	Sequence 307, App
	4	7313	100.0	7313	64	US-10-896-891-30	Sequence 30, Appl
	5	7313	100.0	7313	129	US-60-592-408-133	Sequence 133, App
	6	3910	53.5	7107	41	US-09-948-941-221	Sequence 221, App
	7	3910	53.5	7107	41	US-09-949-003C-1603	Sequence 1603, Ap
	8	3910	53.5	7107	49	US-10-170-235-35981	Sequence 35981, A
	9	3910	53.5	7107	64	US-10-896-891-221	Sequence 221, App
	10	3767	51.5	7312	86	US-60-172-373-5545	Sequence 5545, Ap
	11	3350	45.8	22554	41	US-09-948-941-554	Sequence 554, App
	12	3350	45.8	22554	41	US-09-948-941-745	Sequence 745, App
	13	3350	45.8	22554	41	US-09-949-003C-3997	Sequence 3997, Ap
	14	3350	45.8	22554	41	US-09-949-003C-5293	Sequence 5293, Ap
	15	3350	45.8	22554	64	US-10-896-891-554	Sequence 554, App
	16	3350	45.8	22554	64	US-10-896-891-745	Sequence 745, App
	17	1037	14.2	1210	34	US-09-760-498-104	Sequence 104, App
	18	1037	14.2	1210	48	US-10-143-788-104	Sequence 104, App
C	19	601	8.2	601	41	US-09-948-941-1506	Sequence 1506, Ap
C	20	601	8.2	601	41	US-09-948-941-10216	Sequence 10216, A
C	21	601	8.2	601	41	US-09-949-003C-14347	Sequence 14347, A

c	22	601	8.2	601	41	US-09-949-003C-62838	Sequence 62838, A
c	23	601	8.2	601	64	US-10-896-891-1506	Sequence 1506, Ap
c	24	601	8.2	601	64	US-10-896-891-10216	Sequence 10216, A
c	25	550	7.5	601	41	US-09-947-907-9408	Sequence 9408, Ap
c	26	550	7.5	601	41	US-09-948-941-1503	Sequence 1503, Ap
c	27	550	7.5	601	41	US-09-948-941-10213	Sequence 10213, A
c	28	550	7.5	601	41	US-09-949-003C-14344	Sequence 14344, A
c	29	550	7.5	601	41	US-09-949-003C-62835	Sequence 62835, A
c	30	550	7.5	601	64	US-10-896-891-1503	Sequence 1503, Ap
c	31	550	7.5	601	64	US-10-896-891-10213	Sequence 10213, A
c	32	432	5.9	601	41	US-09-947-907-9407	Sequence 9407, Ap
c	33	432	5.9	601	41	US-09-948-941-1505	Sequence 1505, Ap
c	34	432	5.9	601	41	US-09-948-941-10215	Sequence 10215, A
c	35	432	5.9	601	41	US-09-949-003C-14346	Sequence 14346, A
c	36	432	5.9	601	41	US-09-949-003C-62837	Sequence 62837, A
c	37	432	5.9	601	64	US-10-896-891-1505	Sequence 1505, Ap
c	38	432	5.9	601	64	US-10-896-891-10215	Sequence 10215, A
	39	430	5.9	566	32	US-09-716-990-1050	Sequence 1050, Ap
c	40	423	5.8	599	29	US-09-644-869-8143	Sequence 8143, Ap
	41	414	5.7	415	21	US-09-362-510-13920	Sequence 13920, A
	42	414	5.7	415	21	US-09-362-510A-13920	Sequence 13920, A
	43	414	5.7	415	39	US-09-904-013-13920	Sequence 13920, A
c	44	374	5.1	522	24	US-09-535-897-2429	Sequence 2429, Ap
c	45	360	4.9	601	41	US-09-948-941-1504	Sequence 1504, Ap

Untitled

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 21:12:51 ; Search time 1074 Seconds
(without alignments)
11141.612 Million cell updates/sec

Title: US-09-242-772-116
Perfect score: 7313
Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcgtgcc 7313

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	35	0.5	660	4	US-09-270-767-7626	Sequence 7626, Ap
	3	35	0.5	660	4	US-09-270-767-22908	Sequence 22908, A
c	4	34	0.5	601	4	US-09-949-016-28962	Sequence 28962, A
c	5	34	0.5	601	4	US-09-949-016-125909	Sequence 125909,
c	6	34	0.5	115963	4	US-09-949-016-12298	Sequence 12298, A
c	7	34	0.5	144322	4	US-09-949-016-15316	Sequence 15316, A
c	8	33	0.5	601	4	US-09-949-016-115142	Sequence 115142,
c	9	33	0.5	2398	4	US-09-687-637B-21	Sequence 21, Appl
	10	33	0.5	11730	4	US-09-949-016-14991	Sequence 14991, A
c	11	33	0.5	49416	4	US-09-949-016-15234	Sequence 15234, A
c	12	33	0.5	93364	4	US-09-949-016-14890	Sequence 14890, A
	13	33	0.5	283538	4	US-09-949-016-13506	Sequence 13506, A
	14	32	0.4	1118	4	US-09-439-554-19	Sequence 19, Appl
	15	32	0.4	2075	4	US-09-461-325-130	Sequence 130, App
	16	32	0.4	2075	4	US-10-012-542-130	Sequence 130, App
	17	32	0.4	2075	4	US-10-115-123-130	Sequence 130, App

c	18	32	0.4	100550	4	US-09-949-016-11835	Sequence 11835, A
c	19	32	0.4	100551	4	US-09-949-016-16207	Sequence 16207, A
	20	32	0.4	462589	4	US-09-949-016-12900	Sequence 12900, A
	21	32	0.4	476044	4	US-09-949-016-12412	Sequence 12412, A
c	22	32	0.4	678533	4	US-09-949-016-14577	Sequence 14577, A
c	23	32	0.4	678533	4	US-09-949-016-14578	Sequence 14578, A
	24	31	0.4	286	4	US-10-021-338A-35	Sequence 35, Appl
c	25	31	0.4	321	2	US-08-520-678A-23	Sequence 23, Appl
c	26	31	0.4	321	3	US-08-897-126-23	Sequence 23, Appl
c	27	31	0.4	601	4	US-09-949-016-38299	Sequence 38299, A
	28	31	0.4	601	4	US-09-949-016-53527	Sequence 53527, A
	29	31	0.4	601	4	US-09-949-016-53537	Sequence 53537, A
	30	31	0.4	601	4	US-09-949-016-60222	Sequence 60222, A
c	31	31	0.4	601	4	US-09-949-016-71451	Sequence 71451, A
	32	31	0.4	601	4	US-09-949-016-82033	Sequence 82033, A
	33	31	0.4	601	4	US-09-949-016-82038	Sequence 82038, A
c	34	31	0.4	601	4	US-09-949-016-137776	Sequence 137776,
c	35	31	0.4	601	4	US-09-949-016-146550	Sequence 146550,
c	36	31	0.4	601	4	US-09-949-016-146551	Sequence 146551,
c	37	31	0.4	601	4	US-09-949-016-169981	Sequence 169981,
c	38	31	0.4	601	4	US-09-949-016-189744	Sequence 189744,
	39	31	0.4	997	4	US-09-523-686-1	Sequence 1, Appli
	40	31	0.4	1847	4	US-09-904-615-41	Sequence 41, Appl
	41	31	0.4	2594	4	US-09-602-472A-7	Sequence 7, Appli
	42	31	0.4	2793	4	US-09-602-472A-9	Sequence 9, Appli
	43	31	0.4	3829	2	US-08-631-097-8	Sequence 8, Appli
	44	31	0.4	3829	3	US-08-810-712-6	Sequence 6, Appli
c	45	31	0.4	4741	1	US-07-695-472B-4	Sequence 4, Appli